Amendment to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

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1. (original) A method for analyzing metabolic pathways, comprising:

(a) administering to a subject a substrate labeled with a stable isotope, wherein the relative isotopic abundance of the isotope in the substrate is known;

(b) allowing the labeled substrate to be at least partially metabolized by the subject to form one or more target metabolites; and

(c) determining the abundance of the isotope in a plurality of target analytes in a sample from the subject to determine a value for the flux of each target analyte, wherein the plurality of target analytes comprise the substrate and/or one or more of the target metabolites.

2. (original) The method of claim 1, wherein the determining comprises at least partially separating the target analytes from other biological components in the sample prior to determining the flux values.

3. (original) The method of claim 2, wherein the separating comprises performing a plurality of capillary electrophoresis methods in series.

4. (original) The method of claim 3, wherein the plurality of capillary electrophoresis methods are selected from the group consisting of capillary zone electrophoresis, capillary isoelectric focusing and capillary gel electrophoresis.

5. (original) The method of claim 4, wherein the plurality of capillary electrophoresis methods are selected from the group consisting of capillary zone electrophoresis and capillary isoelectric focusing.

6. (original) The method of claim 5, wherein the performing of the capillary electrophoresis methods comprises performing a plurality of capillary zone electrophoresis methods.

7. (original) The method of claim 3, wherein the performing of the capillary electrophoresis methods generate separate fractions for at least one class of metabolite, wherein the class of metabolite is selected from the group consisting of proteins, polysaccharides, carbohydrates, nucleic acids, amino acids, nucleotides, nucleosides, fats, fatty acids and organic acids.

8. (original) The method of claim 3, wherein the separating comprises conducting a non-electrophoretic separation technique prior to conducting the plurality of electrophoresis methods to precipitate at least some of the biological components.

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9. (currently amended) The method of claim 1, wherein the stable isotope is selected from the group consisting of ^{13}C, ~~^{2}H and ^{15}N.~~ ^{2}H, ^{15}N, ^{18}O, and ^{34}S.

10. (original) The method of claim 1, wherein the substrate is selected from the group consisting of proteins, carbohydrates, nucleic acids, amino acids, nucleotides, nucleosides, fatty acids, organic acids, and fats.

11. (original) The method of claim 10, wherein the substrate is a protein.

12. (original) The method of claim 1, wherein the substrate is a substrate for at least two separate metabolic pathways in the subject, metabolism of the substrate via the at least two metabolic pathways generating at least two byproducts, and wherein the target metabolites comprise the at least two byproducts.

13. (original) The method of claim 1, wherein the sample is obtained from a bodily fluid, the bodily fluid selected from the group consisting of blood, urine, cerebral fluid, spinal fluid, sweat, and gastrointestinal fluids.

14. (original) The method of claim 1, wherein the sample is a cell, a tissue sample or fecal material.

15. (original) The method of claim 1, wherein the determining comprises obtaining multiple samples from the subject at different predetermined time points, separating the target analytes from other biological components in each of the samples, and determining the abundance of the isotope in the target analytes contained in each sample, whereby a plurality of values for the abundance of the isotope in each target analyte are obtained, the flux value for each target analyte being determined from the plurality of abundance values determined for it.

16. (original) The method of claim 1, wherein the target analytes are selected from the group of proteins, carbohydrates, nucleic acids, amino acids, nucleotides, nucleosides, fatty acids, organic acids, and fats.

17. (original) The method of claim 16, wherein the target analyte is a protein.

18. (original) The method of claim 1, wherein the plurality of target analytes comprise the substrate and at least one target metabolite.

19. (original) The method of claim 1, wherein the plurality of target analytes is at least 3 target metabolites.

20. (original) The method of claim 19, wherein the plurality of target analytes is at least 5 target metabolites.

21. (original) The method of claim 1, wherein determination of the abundance of the isotope is performed by mass spectrometry, infrared spectrometry or nuclear magnetic resonance spectrometry.

22. (original) The method of claim 21, wherein determination of the abundance of the isotope is performed by mass spectrometry.

23. (currently amended) The method of claim 2, wherein

~~(a)~~ the stable isotope is 13 C;

~~(b)~~ separating comprises performing a plurality of capillary electrophoresis methods, wherein the plurality of electrophoresis methods are selected from the group consisting of capillary zone electrophoresis, capillary isoelectric focusing and capillary gel electrophoresis; and

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~~(c)~~ the determination of the abundance of the isotope is performed by mass spectrometry.

24. (original) A method for analyzing metabolic pathways, comprising:

(a) separating at least partially a plurality of target analytes from biological components contained in a sample obtained from a subject, the target analytes comprising a substrate labeled with a stable isotope and/or one or more target metabolites resulting from the metabolism of the substrate by the subject, and wherein the relative isotopic abundance of the isotope in the substrate is known; and

(b) determining the abundance of the isotope in a plurality of the target analytes in the sample to determine a value for the flux of each target analyte.

25. (original) The method of claim 24, wherein the separating comprises performing a plurality of capillary electrophoresis methods in series, the capillary electrophoresis methods selected from the group consisting of capillary zone electrophoresis, capillary isoelectric focusing and capillary gel electrophoresis.

26. (original) The method of claim 25, wherein determination of the abundance of the isotope is performed by mass spectrometry

27. (original) A method for screening for metabolites correlated with a disease, comprising:

(a) administering to a test subject and a control subject a substrate labeled with a stable isotope, wherein the relative isotopic abundance of the isotope in the substrate is known and the test subject has the disease;

(b) allowing the labeled substrate to be at least partially metabolized by the test subject and control subject to form one or more target metabolites, and wherein the conditions under which the administering and allowing steps are performed are the same for the test and control subject; and

(c) obtaining a sample from the test and control subject;

(d) determining for each sample the relative abundance of the isotope in a plurality of target analytes to determine a value for the flux of each target analyte, wherein the target analytes comprise the substrate and/or one or more of the target metabolites; and

(e) comparing the values for flux for the test and control subjects, a difference in the flux value for a target analyte in the test subject and corresponding flux value for the control subject indicating that such analyte is potentially correlated with the disease.

28. (original) The method of claim 27, wherein the determining step comprises at least partially separating the target analytes from other biological components in the sample prior to determining the flux values, the separating comprising separately performing a plurality of capillary electrophoresis methods in series with the samples from the test and control subjects.

29. (original) The method of claim 28, wherein the determination of the isotopic abundance is performed by mass spectrometry.

30. (original) The method of claim 27, wherein the disease is selected from the group consisting of cancer, autism, microbial infection and digestive disorders.

31. (original) A method for screening for metabolites correlated with a disease, comprising:

(a) analyzing a sample from a test subject having the disease, the sample comprising a substrate labeled with a stable isotope administered to the test subject and/or one or more target metabolites resulting from metabolism of the substrate by the test subject, the relative isotopic abundance of the isotope in the substrate known at the time of administration, and wherein the analyzing step comprises determining the isotopic abundance of the isotope in a plurality of analytes in the sample to determine a value for the flux of each analyte, wherein the plurality of analytes comprise the substrate and/or one or more of the target metabolites; and

(b) comparing flux values for the analytes with flux values for the same analytes obtained for a control subject, wherein a difference in a flux value for an analyte indicates that such analyte is correlated with the disease.

32. (original) A method for screening for the presence of a disease, comprising:

(a) administering to a test subject a substrate labeled with a stable isotope, wherein the relative abundance of the isotope in the substrate is known;

(b) allowing sufficient time for the labeled substrate to be at least partially metabolized by the test subject to form one or more target metabolites known to be correlated with the disease;

(c) performing a plurality of electrophoretic methods in series to at least partially separate a plurality of target analytes from other biological components in a sample obtained from the test subject, wherein the target analytes comprise the substrate and/or one or more of the target metabolites;

(d) determining a flux value for the target analytes, the flux value for each target analyte being determined from the abundance of the isotope in that analyte; and

(e) comparing determined flux values with corresponding reference flux values for the same target analytes to assess the test subject's risk of disease.

33. (original) The method of claim 32, wherein

(i) if the reference flux values are representative of presence and/or susceptibility to the disease, a statistically significant difference between reference values and test values indicates that the test subject does not have and/or is not susceptible to acquiring the disease; and

(ii) if the reference flux values are representative of absence and/or lack of susceptibility to the disease, a statistically significant difference between reference values and test values indicates that the test subject does have, or is susceptible to acquiring, the disease.

34. (original) The method of claim 33, wherein the plurality of electrophoretic methods are selected from the group consisting of capillary gel electrophoresis, capillary zone electrophoresis and capillary gel electrophoresis.

35. (original) A method for screening for the presence of a disease, comprising:

(a) analyzing a sample from a test subject, the sample comprising a substrate labeled with a stable isotope administered to the test subject and/or one or more target metabolites resulting from metabolism of the substrate by the test subject, the relative isotopic abundance of the isotope in the substrate known at the time of administration, and wherein the analyzing step comprises determining the abundance of the isotope in a plurality of analytes in the sample to determine a value for the flux of each analyte, wherein the plurality of analytes comprise the substrate and/or one or more of the target metabolites; and

(b) for each target analyte, comparing the determined flux value with a range of flux values for that analyte, wherein the range is known to be correlated with the disease and if a determined flux value for a target analyte falls within the range for that target analyte, it indicates that the test subject has the disease or is susceptible to the disease.

36-38. (canceled)

Amendments to the Drawings:

The attached sheet of drawings includes changes to Fig. 11D. This sheet, which includes Figs. 11C and 11D replaces the original sheet including Figs. 11C and 11D.

In Fig. 11D, the value of 136.88 listed in the lower right-hand corner has been corrected from the value of 130.86 as listed on the original drawing sheet.

Attachment: Replacement Sheet
Annotated Sheet Showing Changes